

Amendments to the Specification:

Please replace the paragraph beginning "The primate, e.g., human" at line 1, page 8 with the following amended paragraph:

The primate, e.g., human, gene will encode a small soluble cytokine-like protein[[,]] of about 216 amino acids (for SEQ ID NO: 2) or about 243 amino acids (for SEQ ID NO: 6). See SEQ. ID. NOs: 1, 2, 5, and 6. Exon boundaries are likely to correspond to about 219/220; 393/394; 492/493; and 551/552 of SEQ ID NO:1. Coding segments corresponding to those boundaries are particularly interesting. Translated amino acid sequence, which is encoded by nucleotides 193 to 918 of SEQ ID NO:1, is shown in SEQ ID NO: 2.

Please replace the paragraph beginning "'Derivatives" of IL-D80 or IL-27" at line 6, page 16 with the following amended paragraph:

"Derivatives" of IL-D80 or IL-27 antigens include amino acid sequence mutants from naturally occurring forms, glycosylation variants, and covalent or aggregate conjugates with other chemical moieties, e.g., PEGylation. Covalent derivatives can be prepared by linkage of functionalities to groups which are found in IL-D80 or IL-27 amino acid side chains or at the N- or C-termini, e.g., by standard means. See, e.g., Lundblad and Noyes (1988) *Chemical Reagents for Protein Modification*, vols. 1-2, CRC Press, Inc., Boca Raton, Fla.; Hugli (ed. 1989) *Techniques in Protein Chemistry*, Academic Press, San Diego, Calif.; and Wong (1991) *Chemistry of Protein Conjugation and Cross Linking*, CRC Press, Boca Raton, Fla.

Please replace paragraph beginning "The corresponding rodent" at line 18, page 8 with the following amended paragraph:

The corresponding rodent polynucleotide sequence of IL-D80 is shown in SEQ ID NO: 3. Exon boundaries are likely to run from about 198/199; 360/361; 459/460; and 618/619. The predicted polypeptide sequence, which runs from about nucleotide 199 to 891 of SEQ ID NO: 3, is shown in SEQ ID NO: 4. The predicted signal cleavage site runs from about residue 16-21 of SEQ ID NO: 4; helix A is predicted to run from about residue 21-26 to about residue 41-46; helix B is predicted to run from about residue 72-77 to about residue 101-106; helix C is predicted to run from about residue 108-133 to about residue 141-146; and helix D is predicted to run from about residue 185-190 to about residue 211-215. All positions refer to SEQ ID NO: 4. A variant rodent IL-D80 polynucleotide sequence is shown in SEQ ID NO: 7 and the predicted polypeptide sequence is shown in SEQ ID NO: [[6]] 8. A comparison of rodent IL-D80 (SEQ ID NO: 4) and variant rodent IL-D80 (SEQ ID NO: 8) polypeptide sequences is shown in Figure 2.